
Single-cell mass cytometry adapted to measurements of the cell cycle.

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Public Summary:

Mass cytometry is a new technology that can perform simultaneous analysis of 40 or more parameters in single cells via mass spectrometry and heavy metal conjugated antibodies. It has been successfully utilized for the simultaneous analysis of complex cellular types and intracellular signaling pathways. However, mass cytometry reagents were unavailable for analyzing proliferation and cell cycle, which are critical to the study of cell biology, in particular cancer and tumorigenesis. To address this, Behbehani and coworkers have developed a new methodology for mass cytometry to measure all phases of the cell cycle simultaneously within complex samples, while simultaneously measuring up to 30 additional parameters. The addition of cell cycle analysis greatly increases the utility of mass cytometry for all fields, and will only increase the rate of adoption for this exciting new technology.

Scientific Abstract:

Mass cytometry is a recently introduced technology that utilizes transition element isotope-tagged antibodies for protein detection on a single-cell basis. By circumventing the limitations of emission spectral overlap associated with fluorochromes utilized in traditional flow cytometry, mass cytometry currently allows measurement of up to 40 parameters per cell. Recently, a comprehensive mass cytometry analysis was described for the hematopoietic differentiation program in human bone marrow from a healthy donor. The current study describes approaches to delineate cell cycle stages utilizing 5-iodo-2-deoxyuridine (IdU) to mark cells in S phase, simultaneously with antibodies against cyclin B1, cyclin A, and phosphorylated histone H3 (S28) that characterize the other cell cycle phases. Protocols were developed in which an antibody against phosphorylated retinoblastoma protein (Rb) at serines 807 and 811 was used to separate cells in G0 and G1 phases of the cell cycle. This mass cytometry method yielded cell cycle distributions of both normal and cancer cell populations that were equivalent to those obtained by traditional fluorescence cytometry techniques. We applied this to map the cell cycle phases of cells spanning the hematopoietic hierarchy in healthy human bone marrow as a prelude to later studies with cancers and other disorders of this lineage. (c) 2012 International Society for Advancement of Cytometry.

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